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RAW SEQUENCE LISTING

DATE: 12/23/2002

PATENT APPLICATION: US/09/869,176

TIME: 14:07:24

Input Set : A:\Ocrs3072.app

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3 <110> APPLICANT: TUMER, NILGUN E.
 4 DINMAN, JONATHAN D.
 5 HUDAK, KATALIN A.
 7 <120> TITLE OF INVENTION: VIRUS-RESISTANT TRANSGENIC PLANTS
 9 <130> FILE REFERENCE: OCIRS 3.3-072
 11 <140> CURRENT APPLICATION NUMBER: 09/869,176
 12 <141> CURRENT FILING DATE: 2001-06-26
 14 <150> PRIOR APPLICATION NUMBER: 60/115,791
 15 <151> PRIOR FILING DATE: 1998-12-31
 17 <150> PRIOR APPLICATION NUMBER: PCT/US99/31312
 18 <151> PRIOR FILING DATE: 1999-12-30
 20 <160> NUMBER OF SEQ ID NOS: 14
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1164
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Saccharomyces cerevisiae
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 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (1)..(1161)
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 36 1 5 10 15
 38 ttg cca aga aag aga gct gcc tcc atc aga gct aga gtt aag gct ttt 96
 39 Leu Pro Arg Lys Arg Ala Ala Ser Ile Arg Ala Arg Val Lys Ala Phe
 40 20 25 30
 42 cca aag gat gac aga tcc aag cca gtt gct cta act tcc ttc ttg ggt 144
 43 Pro Lys Asp Asp Arg Ser Lys Pro Val Ala Leu Thr Ser Phe Leu Gly
 44 35 40 45
 46 tac aag gct ggt atg acc acc att gtc aga gat ttg gac aga cca ggt 192
 47 Tyr Lys Ala Gly Met Thr Thr Ile Val Arg Asp Leu Asp Arg Pro Gly
 48 50 55 60
 50 tct aag ttc cac aag cgt gaa gtt gtc gaa gct gtc acc gtt gtt gac 240
 51 Ser Lys Phe His Lys Arg Glu Val Val Glu Ala Val Thr Val Val Asp
 52 65 70 75 80
 54 act cca cca gtt gtc gtt gtt ggt gtt gtc ggt tac gtc gaa acc cca 288
 55 Thr Pro Pro Val Val Val Val Gly Val Val Gly Tyr Val Glu Thr Pro
 56 85 90 95
 58 aga ggt ttg aga tct ttg acc acc gtc tgg gct gaa cat ttg tct gac 336
 59 Arg Gly Leu Arg Ser Leu Thr Thr Val Trp Ala Glu His Leu Ser Asp
 60 100 105 110
 62 gaa gtc aag aga aga ttc tac aag aac tgg tac aag tct aag aag aag 384

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63	Glu	Val	Lys	Arg	Arg	Phe	Tyr	Lys	Asn	Trp	Tyr	Lys	Ser	Lys	Lys	Lys	
64			115					120					125				
66	gct	ttc	acc	aaa	tac	tct	gcc	aag	tac	gct	caa	gat	ggg	gct	ggg	att	432
67	Ala	Phe	Thr	Lys	Tyr	Ser	Ala	Lys	Tyr	Ala	Gln	Asp	Gly	Ala	Gly	Ile	
68		130					135				140						
70	gaa	aga	gaa	ttg	gct	aga	atc	aag	aag	tac	gct	tcc	gtc	gtc	aga	gtt	480
71	Glu	Arg	Glu	Leu	Ala	Arg	Ile	Lys	Lys	Tyr	Ala	Ser	Val	Val	Arg	Val	
72	145					150				155					160		
74	ttg	gtc	cac	act	caa	atc	aga	aag	act	cca	ttg	gct	caa	aag	aag	gct	528
75	Leu	Val	His	Thr	Gln	Ile	Arg	Lys	Thr	Pro	Leu	Ala	Gln	Lys	Lys	Ala	
76				165					170					175			
78	cat	ttg	gct	gaa	atc	caa	ttg	aac	ggg	ggg	tcc	atc	tct	gaa	aag	gtt	576
79	His	Leu	Ala	Glu	Ile	Gln	Leu	Asn	Gly	Gly	Ser	Ile	Ser	Glu	Lys	Val	
80			180					185					190				
82	gac	tgg	gct	cgt	gaa	cat	ttc	gaa	aag	act	gtt	gct	gtc	gac	agc	gtt	624
83	Asp	Trp	Ala	Arg	Glu	His	Phe	Glu	Lys	Thr	Val	Ala	Val	Asp	Ser	Val	
84		195					200				205						
86	ttt	gaa	caa	aac	gaa	atg	att	gac	gct	att	gct	gtc	acc	aag	ggg	cac	672
87	Phe	Glu	Gln	Asn	Glu	Met	Ile	Asp	Ala	Ile	Ala	Val	Thr	Lys	Gly	His	
88		210				215				220							
90	ggg	ttc	gaa	ggg	gtt	acc	cac	aga	tgg	ggg	act	aag	aaa	ttg	cca	aga	720
91	Gly	Phe	Glu	Gly	Val	Thr	His	Arg	Trp	Gly	Thr	Lys	Lys	Leu	Pro	Arg	
92	225			230					235					240			
94	aag	act	cac	aga	ggg	cta	aga	aag	gtt	gct	tgt	att	ggg	gct	tgg	cat	768
95	Lys	Thr	His	Arg	Gly	Leu	Arg	Lys	Val	Ala	Cys	Ile	Gly	Ala	Trp	His	
96			245					250				255					
98	cca	gcc	cac	gtt	atg	tgg	agt	gtt	gcc	aga	gct	ggg	caa	aga	ggg	tac	816
99	Pro	Ala	His	Val	Met	Trp	Ser	Val	Ala	Arg	Ala	Gly	Gln	Arg	Gly	Tyr	
100		260					265				270						
102	cat	tcc	aga	acc	tcc	att	aac	cac	aag	att	tac	aga	gtc	ggg	aag	ggg	864
103	His	Ser	Arg	Thr	Ser	Ile	Asn	His	Lys	Ile	Tyr	Arg	Val	Gly	Lys	Gly	
104		275					280				285						
106	gat	gat	gaa	gct	aac	ggg	gct	acc	agc	ttc	gac	aga	acc	aag	aag	act	912
107	Asp	Asp	Glu	Ala	Asn	Gly	Ala	Thr	Ser	Phe	Asp	Arg	Thr	Lys	Lys	Thr	
108		290				295				300							
110	att	acc	cca	atg	ggg	ggg	ttc	gtc	cac	tac	ggg	gaa	att	aag	aac	gac	960
111	Ile	Thr	Pro	Met	Gly	Gly	Phe	Val	His	Tyr	Gly	Glu	Ile	Lys	Asn	Asp	
112	305			310				315					320				
114	ttc	atc	atg	gtt	aaa	ggg	tgt	atc	cca	ggg	aac	aga	aag	aga	att	gtt	1008
115	Phe	Ile	Met	Val	Lys	Gly	Cys	Ile	Pro	Gly	Asn	Arg	Lys	Arg	Ile	Val	
116			325					330				335					
118	act	ttg	aga	aag	tct	ttg	tac	acc	aac	act	tct	aga	aag	gct	ttg	gaa	1056
119	Thr	Leu	Arg	Lys	Ser	Leu	Tyr	Thr	Asn	Thr	Ser	Arg	Lys	Ala	Leu	Glu	
120			340					345				350					
122	gaa	gtc	agc	ttg	aag	tgg	att	gac	act	gct	tct	aag	ttc	ggg	aag	ggg	1104
123	Glu	Val	Ser	Leu	Lys	Trp	Ile	Asp	Thr	Ala	Ser	Lys	Phe	Gly	Lys	Gly	
124		355					360					365					
126	aga	ttc	caa	acc	cca	gct	gaa	aag	cat	gct	ttc	atg	ggg	act	ttg	aag	1152
127	Arg	Phe	Gln	Thr	Pro	Ala	Glu	Lys	His	Ala	Phe	Met	Gly	Thr	Leu	Lys	

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131 Lys Asp Leu
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145 20 25 30
147 Pro Lys Asp Asp Arg Ser Lys Pro Val Ala Leu Thr Ser Phe Leu Gly
148 35 40 45
150 Tyr Lys Ala Gly Met Thr Thr Ile Val Arg Asp Leu Asp Arg Pro Gly
151 50 55 60
153 Ser Lys Phe His Lys Arg Glu Val Val Glu Ala Val Thr Val Val Asp
154 65 70 75 80
156 Thr Pro Pro Val Val Val Val Gly Val Val Gly Tyr Val Glu Thr Pro
157 85 90 95
159 Arg Gly Leu Arg Ser Leu Thr Thr Val Trp Ala Glu His Leu Ser Asp
160 100 105 110
162 Glu Val Lys Arg Arg Phe Tyr Lys Asn Trp Tyr Lys Ser Lys Lys Lys
163 115 120 125
165 Ala Phe Thr Lys Tyr Ser Ala Lys Tyr Ala Gln Asp Gly Ala Gly Ile
166 130 135 140
168 Glu Arg Glu Leu Ala Arg Ile Lys Lys Tyr Ala Ser Val Val Arg Val
169 145 150 155 160
171 Leu Val His Thr Gln Ile Arg Lys Thr Pro Leu Ala Gln Lys Lys Ala
172 165 170 175
174 His Leu Ala Glu Ile Gln Leu Asn Gly Gly Ser Ile Ser Glu Lys Val
175 180 185 190
177 Asp Trp Ala Arg Glu His Phe Glu Lys Thr Val Ala Val Asp Ser Val
178 195 200 205
180 Phe Glu Gln Asn Glu Met Ile Asp Ala Ile Ala Val Thr Lys Gly His
181 210 215 220
183 Gly Phe Glu Gly Val Thr His Arg Trp Gly Thr Lys Lys Leu Pro Arg
184 225 230 235 240
186 Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly Ala Trp His
187 245 250 255
189 Pro Ala His Val Met Trp Ser Val Ala Arg Ala Gly Gln Arg Gly Tyr
190 260 265 270
192 His Ser Arg Thr Ser Ile Asn His Lys Ile Tyr Arg Val Gly Lys Gly
193 275 280 285
195 Asp Asp Glu Ala Asn Gly Ala Thr Ser Phe Asp Arg Thr Lys Lys Thr
196 290 295 300
198 Ile Thr Pro Met Gly Gly Phe Val His Tyr Gly Glu Ile Lys Asn Asp
199 305 310 315 320

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201 Phe Ile Met Val Lys Gly Cys Ile Pro Gly Asn Arg Lys Arg Ile Val
202           325           330           335
204 Thr Leu Arg Lys Ser Leu Tyr Thr Asn Thr Ser Arg Lys Ala Leu Glu
205           340           345           350
207 Glu Val Ser Leu Lys Trp Ile Asp Thr Ala Ser Lys Phe Gly Lys Gly
208           355           360           365
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213 Lys Asp Leu
214 385
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224 <221> NAME/KEY: CDS
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230 1 5 10 15
232 ctg ccc agg aag cgt gct gcc aga cac agg gga aag gtg aag gca ttc 96
233 Leu Pro Arg Lys Arg Ala Ala Arg His Arg Gly Lys Val Lys Ala Phe
234 20 25 30
236 cca aaa gat gat cca aac aag ccc tgc aag cta act gcc ttc ttg ggc 144
237 Pro Lys Asp Asp Pro Asn Lys Pro Cys Lys Leu Thr Ala Phe Leu Gly
238 35 40 45
240 tac aaa gct ggc atg act cac att gtc aga gat gtt gaa aaa cct gga 192
241 Tyr Lys Ala Gly Met Thr His Ile Val Arg Asp Val Glu Lys Pro Gly
242 50 55 60
244 tca aaa ctc cac aag aaa gag aca tgt gaa gct gtc acc atc att gaa 240
245 Ser Lys Leu His Lys Lys Glu Thr Cys Glu Ala Val Thr Ile Ile Glu
246 65 70 75 80
248 aca cct cca atg gtg att gtt ggt gtt gtt ggg tat gtg aag aca cct 288
249 Thr Pro Pro Met Val Ile Val Gly Val Val Gly Tyr Val Lys Thr Pro
250 85 90 95
252 cgt ggt ctt cgt tgc ctg aac act gtc tgg gct caa cat ctc agt gaa 336
253 Arg Gly Leu Arg Cys Leu Asn Thr Val Trp Ala Gln His Leu Ser Glu
254 100 105 110
256 gag ctt aag agg agg ttc tac aag aac tgg tgc aag tcc aag aag aag 384
257 Glu Leu Lys Arg Arg Phe Tyr Lys Asn Trp Cys Lys Ser Lys Lys Lys
258 115 120 125
260 gcc ttc ttg aaa tac tcc aag aaa tat gaa tct gat gaa ggg aaa aag 432
261 Ala Phe Leu Lys Tyr Ser Lys Lys Tyr Glu Ser Asp Glu Gly Lys Lys
262 130 135 140
264 gac atc cag aca cag ctg gag aaa ttg aag aag tat gca tgc gtc atc 480
265 Asp Ile Gln Thr Gln Leu Glu Lys Leu Lys Lys Tyr Ala Cys Val Ile
266 145 150 155 160
268 cgt gtt ttg gct cac act cag ata agg aag atg aag ggt ctg aaa cag 528

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269 Arg Val Leu Ala His Thr Gln Ile Arg Lys Met Lys Gly Leu Lys Gln
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273 Lys Lys Ala His Leu Met Glu Ile Gln Val Asn Gly Gly Thr Ile Ala
274      180      185      190
276 cag aag gtt gac ttt gca tat ggt ttc ttc gag aag cag gtt cca gtt 624
277 Gln Lys Val Asp Phe Ala Tyr Gly Phe Phe Glu Lys Gln Val Pro Val
278      195      200      205
280 gat gct gtt ttt cag aag gat gag atg att gac atc att ggt gtc acc 672
281 Asp Ala Val Phe Gln Lys Asp Glu Met Ile Asp Ile Ile Gly Val Thr
282      210      215      220
284 aag ggt aag ggt tat gaa ggt gtt gta act cgt tgg ggt gtg aca cgt 720
285 Lys Gly Lys Gly Tyr Glu Gly Val Val Thr Arg Trp Gly Val Thr Arg
286 225      230      235      240
288 ctt cct cgc aaa acc cac agg ggt ctg cgt aag gtt gct tgt att gga 768
289 Leu Pro Arg Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly
290      245      250      255
292 gcc tgg cac cct gct aga gtt tcc tac aca gtt gcc cgt gct ggt caa 816
293 Ala Trp His Pro Ala Arg Val Ser Tyr Thr Val Ala Arg Ala Gly Gln
294      260      265      270
296 aat gga tac cat cac cgt acc gag atg aac aag aag gtt tac aaa cta 864
297 Asn Gly Tyr His His Arg Thr Glu Met Asn Lys Lys Val Tyr Lys Leu
298      275      280      285
300 ggg aag gct ggc caa gag tcc cat gct gct gta act gat ttt gac agg 912
301 Gly Lys Ala Gly Gln Glu Ser His Ala Ala Val Thr Asp Phe Asp Arg
302      290      295      300
304 acc gag aaa gac att act ccc atg ggt gga ttt ccc cat tat ggt gtg 960
305 Thr Glu Lys Asp Ile Thr Pro Met Gly Gly Phe Pro His Tyr Gly Val
306 305      310      315      320
308 gtg aag gat gat tac ctg ttg atc aag gga tgc tgt gtt ggt cct aag 1008
309 Val Lys Asp Asp Tyr Leu Leu Ile Lys Gly Cys Cys Val Gly Pro Lys
310      325      330      335
312 aag agg gtt gta acc ctt cgt cag tcc ctg ctc aac cag acc tct cgt 1056
313 Lys Arg Val Val Thr Leu Arg Gln Ser Leu Leu Asn Gln Thr Ser Arg
314      340      345      350
316 gtc gct ctt gag gag att aag ctg aag ttc atc gat aca tcc tca aag 1104
317 Val Ala Leu Glu Glu Ile Lys Leu Lys Phe Ile Asp Thr Ser Ser Lys
318      355      360      365
320 ttt gga cat ggt cgc ttc cag acc act caa gag aag cag aaa ttc tat 1152
321 Phe Gly His Gly Arg Phe Gln Thr Thr Gln Glu Lys Gln Lys Phe Tyr
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329 <210> SEQ ID NO: 4
330 <211> LENGTH: 389
331 <212> TYPE: PRT
332 <213> ORGANISM: Nicotiana tabacum
334 <400> SEQUENCE: 4

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VERIFICATION SUMMARY

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